



SEQUENCE LISTING

Koontz, Jason
Sklar, Jeffrey

<120> FUSION OF JAZF1 AND JJAZ1 GENES IN
ENDOMETRIAL STROMAL TUMORS

<130> 05311-024001

<140> US 09/874,162

<141> 2001-06-04

<150> US 60/209,093

<151> 2000-06-02

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tgc gga ctc cac ttc ccc acc ctg gcc gac ctc atc gag cac atc gag 153
Cys Gly Leu His Phe Pro Thr Leu Ala Asp Leu Ile Glu His Ile Glu
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gac aac cac atc gat aca gat cca cgg gtt tta gaa aaa caa gaa tta 201
Asp Asn His Ile Asp Thr Asp Pro Arg Val Leu Glu Lys Gln Glu Leu
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cag cag cca acc tat gtt gcc ctg agt tac ata aat aga ttc atg aca 249
Gln Gln Pro Thr Tyr Val Ala Leu Ser Tyr Ile Asn Arg Phe Met Thr
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Asp Ala Ala Arg Arg Glu Gln Glu Ser Leu Lys Lys Lys Ile Gln Pro
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Lys Leu Ser Leu Thr Leu Ser Ser Ser Val Ser Arg Gly Asn Val Ser

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90

95

act ccc cca cgc cac agc agt gga agc ctt act ccc ccc gtg acc cca 393
 Thr Pro Pro Arg His Ser Ser Gly Ser Leu Thr Pro Pro Val Thr Pro
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ccc atc acc ccc tcc tct tca ttc cgc agc agc act ccg aca ggc agc 441
 Pro Ile Thr Pro Ser Ser Ser Phe Arg Ser Ser Thr Pro Thr Gly Ser
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35 40 45
Glu Leu Gln Gln Pro Thr Tyr Val Ala Leu Ser Tyr Ile Asn Arg Phe
50 55 60
Met Thr Asp Ala Ala Arg Arg Glu Gln Glu Ser Leu Lys Lys Lys Ile
65 70 75 80
Gln Pro Lys Leu Ser Leu Thr Leu Ser Ser Val Ser Arg Gly Asn
85 90 95
Val Ser Thr Pro Pro Arg His Ser Ser Gly Ser Leu Thr Pro Pro Val
100 105 110
Thr Pro Pro Ile Thr Pro Ser Ser Phe Arg Ser Ser Thr Pro Thr
115 120 125
Gly Ser Glu Tyr Asp Glu Glu Val Asp Tyr Glu Glu Ser Asp Ser
130 135 140
Asp Glu Ser Trp Thr Thr Glu Ser Ala Ile Ser Ser Glu Ala Ile Leu
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Ser Ser Met Cys Met Asn Gly Gly Glu Glu Lys Pro Phe Ala Cys Pro
165 170 175
Val Pro Gly Cys Lys Lys Arg Tyr Lys Asn Val Asn Gly Ile Lys Tyr
180 185 190
His Ala Lys Asn Gly His Arg Thr Gln Ile Arg Val Arg Lys Pro Phe
195 200 205
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 aggcaggaac cgcg atg gcg cct cag aag cac ggc ggt ggg gga ggg ggc 230
 Met Ala Pro Gln Lys His Gly Gly Gly Gly Gly Gly
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 Gly Ser Gly Pro Ser Ala Gly Ser Gly Gly Gly Gly Phe Gly Gly Ser
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 Ala Ala Val Ala Ala Ala Thr Ala Ser Gly Gly Lys Ser Gly Gly Gly
 30 35 40
 agc tgt gga ggg ggt ggc agt tac tcg gcc tcc tcc tcc tcc tcc gcg 374
 Ser Cys Gly Gly Gly Gly Ser Tyr Ser Ala Ser Ser Ser Ser Ser Ala
 45 50 55 60
 gcg gca gcg gcg ggg gct gcg gtg tta ccg gtg aag aag ccg aaa atg 422
 Ala Ala Ala Ala Gly Ala Ala Val Leu Pro Val Lys Lys Pro Lys Met
 65 70 75

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 80 85 90

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 95 100 105

ata ttt ttg cac aga act ctt act tac atg tct cat cga aac tcc aga 566
 Ile Phe Leu His Arg Thr Leu Thr Tyr Met Ser His Arg Asn Ser Arg
 110 115 120

aca aac atc aaa agg aaa aca ttt aaa gtt gat gat atg tta tca aaa 614
 Thr Asn Ile Lys Arg Lys Thr Phe Lys Val Asp Asp Met Leu Ser Lys
 125 130 135 140

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 145 150 155

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 160 165 170

cca aac tca gaa aat gaa caa aat tct gtt acc ctg gaa gtc ctg ctt 758
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 175 180 185

gtg aaa gtt tgc cac aaa aaa aga aag gat gta agt tgt cca ata agg 806
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caa gtt ccc aca ggt aaa aag cag gtg cct ttg att cct gac ctc aat 854
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 225 230 235

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 Phe Glu Pro Ser Asn Ser His Met Val Lys Ser Tyr Ser Leu Leu Phe
 240 245 250

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 255 260 265

gaa acc aat gaa aat att gat gtc aat gaa gag ctt cca gcc aga aga 1046
 Glu Thr Asn Glu Asn Ile Asp Val Asn Glu Glu Leu Pro Ala Arg Arg
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Val Phe Asp Lys Asn Arg Arg Leu Gln Leu Leu Asp Gly Glu Tyr Glu	
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Thr Trp Glu Thr Ile Leu Asp Gly Lys Arg Leu Pro Pro Phe Glu Thr	
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Phe Ser Gln Gly Pro Thr Leu Gln Phe Thr Leu Arg Trp Thr Gly Glu	
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Thr Asn Asp Lys Ser Thr Ala Pro Ile Ala Lys Pro Leu Ala Thr Arg	
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Phe Tyr Gln Phe Leu Tyr Asn Asn Asn Thr Arg Gln Gln Thr Glu Ala	
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Arg Asp Asp Leu His Cys Pro Trp Cys Thr Leu Asn Cys Arg Lys Leu	
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Glu Cys Tyr Asp Gly Ser Tyr Ala Gly Asn Pro Gln Asp Ile His Arg	
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A3

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625 630 635	
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A3

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 Gly Gly Ser Tyr Ser Ala Ser Ser Ser Ser Ala Ala Ala Ala Ala
 50 55 60
 Gly Ala Ala Val Leu Pro Val Lys Lys Pro Lys Met Glu His Val Gln
 65 70 75 80
 Ala Asp His Glu Leu Phe Leu Gln Ala Phe Glu Lys Pro Thr Gln Ile
 85 90 95
 Tyr Arg Phe Leu Arg Thr Arg Asn Leu Ile Ala Pro Ile Phe Leu His
 100 105 110
 Arg Thr Leu Thr Tyr Met Ser His Arg Asn Ser Arg Thr Asn Ile Lys
 115 120 125
 Arg Lys Thr Phe Lys Val Asp Asp Met Leu Ser Lys Val Glu Lys Met
 130 135 140

Lys Gly Glu Gln Glu Ser His Ser Leu Ser Ala His Leu Gln Leu Thr
 145 150 155 160
 Phe Thr Gly Phe Phe His Lys Asn Asp Lys Pro Ser Pro Asn Ser Glu
 165 170 175
 Asn Glu Gln Asn Ser Val Thr Leu Glu Val Leu Leu Val Lys Val Cys
 180 185 190
 His Lys Lys Arg Lys Asp Val Ser Cys Pro Ile Arg Gln Val Pro Thr
 195 200 205
 Gly Lys Lys Gln Val Pro Leu Ile Pro Asp Leu Asn Gln Thr Lys Pro
 210 215 220
 Gly Asn Phe Pro Ser Leu Ala Val Ser Ser Asn Glu Phe Glu Pro Ser
 225 230 235 240
 Asn Ser His Met Val Lys Ser Tyr Ser Leu Leu Phe Arg Val Thr Arg
 245 250 255
 Pro Gly Arg Arg Glu Phe Asn Gly Met Ile Asn Gly Glu Thr Asn Glu
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Cys Gly Leu His Phe Pro Thr Leu Ala Asp Leu Ile Glu His Ile Glu	
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Pro Ile Thr Pro Ser Ser Ser Phe Arg Ser Ser Thr Pro Thr Glu Pro	
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A3

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 660 665 670

A3

Cys	Met	Leu	Phe	Val	Glu	Asn	Tyr	Gly	Gln	Lys	Ile	Ile	Lys	Lys	Asn
	675						680					685			
Leu	Cys	Arg	Asn	Phe	Met	Leu	His	Leu	Val	Ser	Met	His	Asp	Phe	Asn
	690					695					700				
Leu	Ile	Ser	Ile	Met	Ser	Ile	Asp	Lys	Ala	Val	Thr	Lys	Leu	Arg	Glu
705					710				715						720
Met	Gln	Gln	Lys	Leu	Glu	Lys	Gly	Glu	Ser	Ala	Ser	Pro	Ala	Asn	Glu
			725					730						735	
Glu	Ile	Thr	Glu	Glu	Gln	Asn	Gly	Thr	Ala	Asn	Gly	Phe	Ser	Glu	Ile
		740						745					750		
Asn	Ser	Lys	Glu	Lys	Ala	Leu	Glu	Thr	Asp	Ser	Val	Ser	Gly	Val	Ser
	755					760						765			
Lys	Gln	Ser	Lys	Lys	Gln	Lys	Leu								
	770					775									

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 <211> 2328
 <212> DNA
 <213> Homo sapiens

A3

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	tcattccgca	gcagcactcc	gacagagcca	acacagatct	atagattttct	tcgaactcgg	420
	aatctcatag	caccaatatt	tttgacacaga	actcttactt	acatgtctca	tcgaaactcc	480
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<220>
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<220>
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<210> 12
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<212> DNA
<213> Artificial Sequence

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<220>
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<400> 12
atcaccccct cctcttcatt 20

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<210> 13
<211> 20
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<220>
<223> primer for PCR

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<400> 13
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<210> 14
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<213> Artificial Sequence

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<220>
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<400> 14

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22

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<210> 16

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22

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 17

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21

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 18

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20

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

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A3

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<220>
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<220>
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<220>
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